

FIGURE 34

GCCGCGGCGAGAGCGCGCCAGCCCCGCGCGGATGCCCGCGCGCCAGGACGCCTCCTCCGCTGCTGGCCCCGGC
CGGCGGCCCTGACTGCTGCTGCTGCTGCTGCTGCGGCATGGCGGCGCGCGGCGCTGGGCGCGCCGCGGCCAGG
AGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGACGCGGAGGACCGCGCACAGCAAGCAGCACC
TGTCACGCGCGGACATGTTACGCGACGGGATCCAGAGCGCGCGCGCACTTCGTATGTTCTTCGCGCCCTGGTGTG
GACATCTGCGCAGCGCTGCGCGCGACTTGGAAATGACCTGGGAGACAAATACAAACAGATGGAAAGATGCCAAAGTCT
ATGTGGCTAAAGTGGACTGCAAGCGCCCACTCCGACGTGTGCTCCGCCAGGGGGTGCAGGATACCCCACTTAA
AGCTTTTCAAGCCAGGCCAAGAGAGCTGTGAAGTACAGGGTCTCTCGGACTTCCAGACACTGGAAAACTGGATGC
TGCAGACACTGAACGAGGAGCCAGTGACACAGAGCCGGAAGTGAACCGCCAGTGCCCCGAGCTCAAGAACG
GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCAACAAGGCGAACCTTTATCAAGTTCTTCGCTC
CTGGTGTGGTCACTGCAAGGCCCTGGCTCCAACTTGGGAGCAGCTGGCTCTGGGCTTTGAACATTCGAAAACTG
TCAAGATTGGCAAGGTTGAATTGTACACAGCACTATGAACTCTGCTCCGGAACACAGGTTCTGGTCTATCCCACTC
TTCTCTGTTTCCGAGATGGGAAAAAGGTGGATCAGTACAAGGGAAAGCGGGATTGGAGTCACTGAGGGAGTACG
TGGAGTCGCACTGCAAGCGCACAGAGACTGGAGCGACGAGACCGTACGCGCTCAGAGGCCCGCGGTCTGGCAG
CTGAGCCGAGGCTGACAAAGGCGACTGTGTTGGCACTCACTGAAATAAATTCGATGACACATTGCGAAGGAA
TAACCTTCATCAAGTTTATGCTCCATGGTGTGGTCATTGTAAGACTCTGGCTCCTACTTGGGAGGAACCTCTA
AAAAGGAATTCCTGGTCTGGCGGGGGTCAAGATCGCGAAGTAGACTGCACTGCTGAACGGAATATCTGCAGCA
AGTATTCGGTACGAGGCTACCCCACTGTTATGCTTTTCCGAGGAGGGAAGAAAGTCACTGAGCACAGTGGAGGCA
GAGACCTTGACTCGTTACACCGCTTTGCTCAGGCAAGCGAAAGACGAACCTTAGGAACACAGTTGGAGGTTCAC
CTCTCCTGCCAGCTCCCGCACCTTGGCTTTAGGAGTTCAGTCCACAGAGGCCACTGGGTTCCAGTGGTGGCT
GTTTCAAGAGCAGAACATACTAAGCGTGAAGGTATCTTCTTGTGTGTGTTTTCACAGCCCAACCACTCTACAG
ATTCTTTTAAAGTTAAAGTTTCTTAAGTAAATGTGAACCTCATGGTCACTTTGTGTAACACTTTCACTGGGATA
TATCCCTTTGACTCTCTCTGATGAAATTTACATGGTTTCCCTTTGAGACTAAATAGCGTTGAGGGAAATGAA
TTGCTGAGCAATTTTGTGCTCTGATGTTGATGATTGTTGGTGAAGAAAGCACATCCAAAGCAATAGTTTCACTGC
CCACGAGTTTCGGAAGGTTGGCTTGTGGCAGTATGACGTTCTCTGATCTTAAGTCAACAGTTGACTCAATAC
TGTGTGGTCTCGATAGACTGAGCAGATTGAAATGCAAAACCACACTCTGGAAGATACCTTCAAGCGCGCTGC
TGGAGCTCTGTTGCTGTGAATACCTTCTCTAGTGTGAGAGGTTAGCCGTGATGAAGACGCGTTACTCTGACC
GTGCTGATGAAGAGATGCTGATGGCCATACTTTATGTGTGATACTTGTCAAATCAGTTACTGTTTCAAGGAGT
CCTCTGTTTCTCAGCGGGTAGGCGATGGAATAATCCACAGGCTCATTCTCAGTATCTCATTAACTCATTGA
AAGATTCCAGTTGATTTGTCACTGGGGTGACAAGACGAGCAGGCTTTCCAGGCTCGGGTATCCAGGGAGGC
TCTGACGCGCTGTGAAGGGCCCTTAACAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCTTTTAGAGG
CTTGCTATCTGTTGCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAATGGGATGCATTGATCTCAAGAC
CAAGACAGATGTCACTGGGCTGCTCTGGCCCTGTGTGACAGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTTA
ACTCATGCTGTCTTGTGATTAAACACTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA
GATAGGTGTTTGTCTTTTACCATCGAGTACTTCCCAATAAACCCTTTGATCCAAACACTCTTCAACCACT
CCCATACGCAAGGGGATGGGATACTTGGCCAAAGTAACTGTGTGTAGGAATCTTAGAAACAGAACCTTATA
CTGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACAGGCTCTGCTTTAAAGGAAATCTTTATTAATCAG
TATGGTTTACAGATAATCTTTTAAAAAAACCACCTCTAGAGAAGCAACTGTCAAGAGTCTTGTGACA
CACAACTTCAGCTTGTACACAGAGTCTGTATTCCAGAAAAATCAAGTGGTACAATTTGTTGTTTACACTAT
GATACCTTCTAAATAAATCTTTTAAAA

09978295.101501

Abstract

```
><subunit 1 of 1, 432 aa, 1 stop
```

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLLPLLARPAALTALLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLTYTADMPTHGIQSAAHFVMMFAPWCGHCQRLQPTWNLDGKYNSMEDAKVYVAKVDCTAH
SDVCSAQGVRGYP TLKLFKPGQEA VKYQGPRDFQTLENWMLQTLNEEPVTPPEPEVEPPSAPE
LKQHYLYELASASN FELHVAQGDHF IKFFAPWCGCHKALAPTWEQLALGLEHSETVKIGKVDCT
QHLYELCSGNQVRGYPTLLWFRDGGKKVDQYKGRDLSEYELAPVEYESQLQRTTETGATETVPTPSEA
PVLAAEPBADKGTVLALTENNPDDTIAEGITFIKFSAPCGCKTLAPTWEELSKEFFPGLA
GVKIAEVDCTAERN ICSKYSVRGYPTLLWFRDGGKKVSEHSGGRDLDSLHFRVLSOAKDEL

Signal sequence:

amino acids 1-32

FIGURE 36

CTTTTCTGAGGAACACAGCAAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA
CCGCTGAAGTCTGTGCCACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGC'TTGGAATACCTGGAGAAAAAGGCAAGCAGGTACT
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTTTTCGGGTGTTTATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA
TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT
ACGTATTTGCTATTTTCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTCCTG
ATTGTACTACATTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAAA

10373295.10501